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RAW SEQUENCE LISTING PATENT APPLICATION US/09/079,569

DATE: 07/30/98 TIME: 10:19:28

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This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED SEQUENCE LISTING 1 2 General Information: 3 (1) 5 (i) APPLICANT: Boyle, William J. 6 7 (ii) TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS 8 (iii) NUMBER OF SEQUENCES: 7 9 10 11 (iv) CORRESPONDENCE ADDRESS: 12 (A) ADDRESSEE: Amgen Inc. (B) STREET: 1840 Dehavilland Drive 13 14 (C) CITY: Thousand Oaks (D) STATE: California 15 16 (E) COUNTRY: USA 17 (F) ZIP: 91230-1789 18 (v) COMPUTER READABLE FORM: 19 20 (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible 21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 22 23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 24 (vi) CURRENT APPLICATION DATA: 25 (A) APPLICATION NUMBER: 09/079,569 26 (B) FILING DATE: 27 (C) CLASSIFICATION: 28 29 30 (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/842,842 31 32 (B) FILING DATE: 33 34 (viii) ATTORNEY/AGENT INFORMATION: 35 (A) NAME: Winter, Robert B. (C) REFERENCE/DOCKET NUMBER: A-451 36 37 38 (2) INFORMATION FOR SEQ ID NO:1: 39 40 41 (i) SEQUENCE CHARACTERISTICS: 42 (A) LENGTH: 52 base pairs 43 (B) TYPE: nucleic acid 44 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

RAW SEQUENCE LISTING PATENT APPLICATION US/09/079,569

DATE: 07/30/98 TIME: 10:19:30

INPUT SET: S3286.raw (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: GTTCTCCTCA TATGGATCCA AACCGTATTT CTGAAGACAG CACTCACTGC TT (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: TACGCACTCC GCGGTTAGTC TATGTCCTGA ACTTTGA (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 53 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: GTTCTCCTCA TATGAAACCT GAAGCTCAAC CATTTGCACA CCTCACCATC AAT (2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 45 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA

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103	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
104	(MI) DECEMBE DECEMENTATION. DEC 15 No. 1.	
	CEMPORICE CONTROL TRANSPORTED A CENTRALA COLOR CONTROL	4.5
105	GTTCTCCTCA TATGCATTTA ACTATTAACG CTGCATCTAT CCCAT	45
106		
107	(2) INFORMATION FOR SEQ ID NO:5:	
108		
109	(i) SEQUENCE CHARACTERISTICS:	
110	(A) LENGTH: 59 base pairs	
111	(B) TYPE: nucleic acid	
112	(C) STRANDEDNESS: single	
113	(D) TOPOLOGY: linear	
114		
115	(ii) MOLECULE TYPE: cDNA	
116		
117		
118		
119		
120	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
121	(XI) SECONCE DESCRIPTION. SEC ID NO.3.	
	CEMOCROCIMO TEMOS CENTRE EN COCENCIA CENTROCONES COCENTROCONES EN CARROLLES	
122	GTTCTCCTCA TATGACTATT AACGCTGCAT CTATCCCATC GGGTTCCCAT AAAGTCACT	59
123		
124	(2) INFORMATION FOR SEQ ID NO:6:	
125		
126	(i) SEQUENCE CHARACTERISTICS:	
127	(A) LENGTH: 2295 base pairs	
128	(B) TYPE: nucleic acid	
129	(C) STRANDEDNESS: single	
130	(D) TOPOLOGY: linear	
	(b) TOPOLOGI: IIIIear	
131		
132	(ii) MOLECULE TYPE: cDNA	
133		
134		
135	(ix) FEATURE:	
136	(A) NAME/KEY: CDS	
137	(B) LOCATION: 1581105	
138	(-)	
139		
	() GEOVENOR DECORIDATION, GEO. ID NO. C.	
140	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
141		
142	GAGCTCGGAT CCACTACTCG ACCCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG	60
143		
144	CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA	120
145		
146	TCGCGGAGCA GGGCGCCCGA ACTCCGGGCG CCGCGCC ATG CGC CGG GCC AGC CGA	175
147	Met Arg Arg Ala Ser Arg	
148	1 5	
149	<u>.</u>	
150	מאר שאר ככב אאכ שאר כשב ככב אבם שבם כאם מאם אשם ככב אבם ככב	222
	GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC	223
151	Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro	
152	10 15 20	

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153 154 155 156 157								CCG Pro			271
158 159 160 161								CTC Leu			319
162 163 164 165								CTG Leu			367
166 167 168 169								ACT Thr 85			415
170 171 172 173								CAG Gln			463
174 175 176 177								AGG Arg			511
178 179 180 181								ATT Ile			559
182 183 184 185								TCA Ser			607
186 187 188 189								GCA Ala 165			655
190 191 192 193								GTC Val			703
194 195 196 197								AAC Asn			751
198 199 200 201								TAT Tyr			799
202 203 204 205								AGC Ser		-	847

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CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTATA CAG ATC AGC ATC Pro Thr Asp Tyr Leu Gin Leu Met Val Tyr Val Val Lys Thr Ser Ile 245															77	ידינומוז	err.	C2206	
Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 240 245 245 240 245	225	aam	202	~~~		amm.	~~	ama	3 mg	ama.		ama	amm.					33200.FC	
208																			895
209		Pro	Inr	Asp	Tyr		GIN	ьeu	Met	vaı	_	vaı	vaı	гаг	Thr		тте		
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250 255 260 261 261 262 262 263 263 263 263 263 263 263 263 265 270 275																			943
1315 165 TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA 991 175		Lys	Ile	Pro		Ser	His	Asn	Leu		Lys	Gly	GIY	Ser		Lys	Asn		
214 TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA 991 215 TTP Ser Gly Ash Ser Glu Phe His Phe Tyr Ser Ile Ash Val Gly Gly 265 270 275 217 TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC 1039 219 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Ash 280 280 290 221 CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC 1087 1087 222 CCT TCC CTG CTG GAT CCG GAT CAA GAT GCA CAA GAT TTT GGG GCT TTC 1087 1087 223 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe 295 310 310 225 AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG 1135 1135 226 Lys Val Gln Asp Ile Asp 315 1195 227 Lys Val Gln Asp Ile Asp 315 1195 228 ACTAAGAGAC ATGTTTGGAAA CTCTTTAAAA AATGGATGAT GTCTATACAT GTGTAACAT 1195 231 ACTAGAGAGA ATGTACACAG GTGTATGAAA CTCACAGCCC TCTCTTTGA GCCTGTACAG 1255 232 ACTAGTTTT AATGTTTC TAGAATTGAA CCAGTGAGT ATGGAAGGATTAC CAACAGTTTT 1315 235					250					255					260				
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216	214																		991
217	215	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	Gly		
218 Phe Phe Lys Leu Arg Ala Gly Glu Glu Glu Ile Ser Ile Gln Val Ser Asn 280 280 285 290 285 280 285 290 285 290 285 290 285 290 285 290 285 290 285 290 285 286 295 295 295 295 295 295 295 295 295 295	216			265					270					275					
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220 280 285 290 221 222 CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC 223 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe 225 300 305 310 225 226 AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG 227 Lys Val Gln Asp Ile Asp 228 315 229 220 ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT 231 ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTGA GCCTGTACAG 232 ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG 233 CAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGG GAGGTATTC CGATGCTTAT 236 ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGG AGAGGTATTC CGATGCTTAT 237 CGAAAACTTA CACGTGAGCT ATGGAAGGG GTCACAGTCC CTGGGTCTAA CCCCTGGACA 240 TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC CTGGGTCTAA AATGATAGTG 241 TTCTAAATGA GGAGAGAAA ATAATGTAT TTTTATATAA TGTCTAAAGT TATATTTCAG 242 TTCTAAATGA GGAGAGAAA ATAATATGTAT TTTTATATAA TGTCTAAAGT TATATTTCAG 243 TTTCTAAATGA GAGAGGAAA ATTATATGTAT TTTTATATAA TGTCTAAAGT TATATTTCAG 244 TTTCTAATGA GAGAGAGAAA ATATATGTAT TTTTATATATT TAAATGTAC GATGATTTA 245 GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTT TAAATGTAC GATGATTTA 246 GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTT TAAATGTAC GATGATTTA 247 AATATTTAAA AATGTCCCC TGTTGACATA TTTAATGTTT TAAATGTAC GATGATTTA 248 AATATTTAAA AATGTCCCC TGTTGACATA TTTAATGTTT TAAATGTAC GATGATTTA 249 ACTGGTGCAC TTTGTAATTC CCCTGAAGGT ACCGTAGCT AAGGGGCCAG AATACTGTTT 250 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TAAATGAGT CTTCAGACTT 251 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TAAATGAGT CTTCAGACTT 252 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TAAATAAAATA																			
221 CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC 23 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe 24 295 300 305 310 255 26 AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG 27 Lys Val Gln Asp Ile Asp 28 315 29 ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT 31 ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG 31 ACTAGAGAGAC ATGGACCACG GTGTATGAAA CCAGAGCCC TCTCTCTTGA GCCTGTACAG 323 ACTAAGAGAC ATGGACCACG GTGTATGAAA CCAGAGTCT GGTGATTACA CAACGGTTTT 1315 235 ACAATTTTGT AATGATTCC TAGAATTGAA CCAGACTCT CTGGGTCTAA CCCCTGGACA 1435 236 ACAAATTTGT AATGATTCC TAGAATTGAA CCAGATTGG AGAGGTATC CGATGCTTAT 1375 237 AGAAAACTTA CACGTGAGCT ATGGAAGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA 1435 239 TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 1495 240 TGTGCCACTG AGAACCTTGA AATTATAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 1495 241 TTCTAAATGA GGAGAGAAAA ATAATATGTAT TTTTATATAA TGTCTAAAGT TATATTTCAG 1615 242 TGAAGGGTTA AGTTCTTTTG AATTGTTAA ATTATATTTG TGCTATAGAT TTTGATTCAA 1675 243 ATATTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTAC GATGTATTTA 1735 244 ATATTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTAC GATGTATTTA 1735 245 ACTGGTGACA CATGTAGTTT ATTTCTTATA TCTTTTTAAC TTAATAGGT CTTCAGACTT 1795 251 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TTAATAGGT CTTCAGACTT 1855 252 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TTAATAGGT CTTCAGACTT 1855 253 GTCAAAACTA TGCAAGCAAA ATAAATAAAT AAAATAAAA TGAATACCTT GAATAATAAG 1915 255 TAGGATGTT GTCACCAGGT GCCTTTCAAA TTTAAGAGCT AATTGACTTT AGGAGCTGAC 1975 257 TAGGATGTT GTCACCAGGT GCCTTTCAAA TTTAAGAGCT AATTGACTTT AGGAGCTGAC 1975 257 TAGGATGTT GTCACCAGGT GCCTTTCAAA TTTAAGAAGCT AATTGACTTT AGGAGCTGAC 1975 257 TAGGATGTT GTCACCAGGT GCCTTTCAAA TTTAAGAAGCT AATTGACTTT AGGAGCTGAC 1975 257 TAGGATGTT GTCACCAGGT GCCTTTCAAA TTTAAGAGCT AATTGACTTT AGGAGCTGAC 1975				_,_		5													
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224 295 300 305 310 225 AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG Lys Val Gln Asp Ile Asp 227 Lys Val Gln Asp Ile Asp 228 315 230 ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT 231 ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG 232 ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG 233 CACAATTTTGT AATGATTCC ATAGGTGAT GTAGATTCAT GGTGATACAC CAACGGTTT 231 ACAATTTTGT AATGATTCC TAGAATTGAA CCAGATTGG AGAGGTATTC CGATGCTTAT 232 ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGG AGAGGTATTC CGATGCTTAT 233 GAAAAACTTA CACGTGAGCT ATGGAAGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA 234 TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 240 TGTGCCACTG AGAACCTTGA AATTATAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 241 TTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTCAG 242 TGAAGGGTTA AGTTCTTTTG AATTGTTACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTTT 243 TTTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTCAG 244 TTTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATATA																			1067
AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG Lys Val Gln Asp 11e Asp 315 229 330 ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT 1195 231 ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG 1255 233 GACAATTTGT AATGATTCC TAGAATTGAA CCAGATTGG AGAGGTATTC CGATGCTTAT 1315 235 ACAATTTTGT AATGATTCC TAGAATTGAA CCAGATTGG AGAGGTATTC CGATGCTTAT 1375 236 ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGG AGAGGTATTC CGATGCTTAT 1375 237 CGAGGGTTA AGTCTTTTG AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 1495 240 TGAGAGGGTTA AGTTCTTTTG AATTGTTACA TTGCGCTGG ACCTGCAAAT AAGTTCTTTT 1555 241 TTCTTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTTCAG 1615 242 GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGAT TTTGATTCAA 1675 243 AATATTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTAC GATGTATTTA 1735 244 ATATTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTACA GATGTATTTA 1735 245 ACTGGTGCAC TTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT 1795 251 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TTAATAGAGT CTTCAGACTT 1795 252 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TTAATAGAGT CTTCAGACTT 1795 253 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAAC TTAATAGAGT CTTCAGACTT 1795 254 GTCAAAACTA TGCAAGCAAA ATAAATAAAT AAAATAAAA TGAATACCTT GAATAATAAG 1915 255 CTGGTGACCA CATGTAGTTT ATTTCTTTAA ATTAGAAGCT AATTGACTTT AGGAGCTGAC 1975 256 TAGGATGTTG GTCACCAGGT GCCTTTCAAA TTTAGAAGCT AATTGACTTT AGGAGCTGAC 1975	_		ser	ьeu	Leu	Asp		Asp	GIII	Asp	Ala		TYL	PHE	GIY	Ala			
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Lys Val Gln Asp Ile Asp 228 230 ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT 231 232 ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC TCTCTCTGA GCCTGTACAG 233 234 GTTGTGTATA TGTAAAGTCC ATAGGTGATG TTAGATTCAT GGTGATACA CAACGGTTTT 235 ACAATTTGT AATGATTCC TAGAATTGAA CCAGATTGG AGAGGTATTC CGATGCTTAT 237 238 GAAAAACTTA CACGTGAGCT ATGGAAGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA 1435 239 240 TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 241 242 TGAAGGGTTA AGTTCTTTTG AATTGTTACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTT 1555 243 244 TTTCTAATGA GGAGGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTCAG 245 246 GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGTA TTTGATTCAA 247 248 AATATTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTAC GATGATTTA 249 249 ACTGGTGCAC CTTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGCAG AATACTGTTT 1795 251 252 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTAAC TTAATAGAGT CTTCAGACTT 1855 253 254 GTCAAAACTA TGCAAGCAAA ATAAATAAAT AAAATAAAA TGAATACCTT GAATAATAG 1915 255 TAGGATGTTG GTCACCAGGT GCCTTTCAAA TTTAGAAGCT AATTGACTTT AGGAGCTGAC 1975																_		_	
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233 234 GTTGTGTATA TGTAAAGTCC ATAGGTGATG TTAGATTCAT GGTGATTACA CAACGGTTTT 1315 235 236 ACAATTTTGT AATGATTCC TAGAATTGAA CCAGATTGGG AGAGGTATTC CGATGCTTAT 1375 237 238 GAAAAACTTA CACGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA 1435 239 240 TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG 1495 241 242 TGAAGGGTTA AGTTCTTTTG AATTGTACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTTT 1555 243 244 TTTCTAATGA GGAGAGAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTTCAG 1615 245 246 GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGTA TTTGATTCAA 1675 247 248 AATATTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTACA GATGTATTTA 1735 249 250 ACTGGTGCAC TTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT 1795 251 252 CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTTAC TTAATAGAGT CTTCAGACTT 1855 253 254 GTCAAAACTA TGCAAGCAAA ATAAATAAAT AAAAATAAAA TGAATACCTT GAATAATAAG 1915 255 TAGGATGTTG GTCACCAGGT GCCTTTCAAA TTTAGAAGCT AATTGACTTT AGGAGCTGAC 1975	231																		
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240TGTGCCACTGAGAACCTTGAAATTAAGAGGATGCCATGTCATTGCAAAGAAATGATAGTG1495241TGAAGGGTTAAGTTCTTTTGAATTGTTACATTGCGCTGGGACCTGCAAATAAGTTCTTTT1555243TTTCTAATGAGGAGAGAAAAATATATGTATTTTTATATAATGTCTAAAGTTATATTTCAG1615245GTGTAATGTTTTCTGTGCAAAGTTTTGTAAATTATATTTGTGCTATAGTATTTGATTCAA1675247AATATTTAAAAATGTCTCACTGTTGACATATTTAATGTTTTAAATGTACAGATGTATTTA1735249ACTGGTGCACTTTGTAATTCCCCTGAAGGTACTCGTAGCTAAGGGGGCAGAATACTGTTT1795250ACTGGTGACCACATGTAGTTTATTTCTTTATTCTTTTTAACTTAATAGAGTCTTCAGACTT1855251GTCAAAAACTATGCAAGCAAAATAAATAAATAAAAATAAAATGAATACCTTGAATAATAAG1915255TAGGATGTTGGTCACCAGGTGCCTTTCAAATTTAGAAGCTAATTGACTTTAGGAGCTGAC1975257		0			C11CC.	. 00.			.000	. 01	011011	J	010	3010.				-	1133
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